AMENDMENTS TO THE CLAIMS

1. **(Canceled)**

2. **(Currently amended):** ~~The method of claim 1,~~ A method for estimating the precision of measurements taken from an array, comprising:

(a) identifying a set of low-level data measurements;

(b) estimating a standard deviation, σ_ε of an additive error component, ε ;

(c) estimating a background parameter, α ;

(d) identifying a set of replicated high-level data measurements;

(e) estimating a standard deviation, σ_η , of a proportional error component, η from the standard deviation of the logarithm of the replicated high-level data set;

(f) measuring a signal, y, wherein said signal indicates an amount of a biological molecule; and

(g) estimating a variance of the measured signal as

$$Var\{y\} = \mu^2 e^{\sigma_\eta^2}\left(e^{\sigma_\eta^2} - 1\right) + \sigma_\varepsilon^2$$

wherein μ is the amount of the biological molecule and

$$y = \alpha + \mu e^{\eta} + \varepsilon$$

and wherein said identifying step (a) comprises the use of a thresholding algorithm to establish a cutoff, and the set of low-level data consists of those data with values less than the cutoff.

3. (Previously amended): The method of claim 2, wherein the thresholding algorithm comprises the steps of:

(a) identifying A_N, an initial set of low-level data measurements consisting of q percent of the total number of data points having the lowest measurement values, $A_N = \{x_1, x_2, \ldots, x_{no}\}$;

(b) calculating a mean and a standard deviation of the initial set;

(c) calculating a cutoff point, u_N = mean plus (c × the standard deviation), wherein $2 \leq c \leq 3$;

(d) defining a new set, $A_{N+1} = \{x_j < u_N\}$;

(e) calculating a mean and standard deviation of the new set; and

(f) repeating steps (c) and (d) using the mean and standard deviation of the new set until the algorithm converges.

4. (Previously amended): The method of claim 2, wherein the thresholding algorithm comprises the steps of:

(a) identifying A_N, an initial set, of low-level data consisting of q percent of the total number of data points having the lowest measurement values, $A_N = \{x_1, x_2, \ldots, x_{no}\}$;

(b) calculating a median of the initial set, $m_0 = \text{median } \{x_j\}_{j=1}^{n_o}$ and a median of the absolute deviations about the median, $MAD_0 = \text{median } \{|x_j - m_o|\}_{j=1}^{n_o}$;

(c) calculating a cutoff point, $u_0 = MAD_0 + (c \times s_0)$, wherein $s_0 = MAD_0/0.675$ and $2 \leq c \leq 3$;

(d) defining a new set, $A_{N+1} = \{x_j < u_N\}$;

(e) calculating a median and a median of the absolute deviations about the median of the new set; and

(f) repeating steps (c) and (d) using the median and the median of the absolute deviations about the median of the new set until the algorithm converges.

5. (Original): The method of claim 2, wherein the mean of the low-level data measurements is used as the estimate of the background parameter, α.

6. **(Currently amended):** The method of claim 2 ~~claim 1~~, wherein the standard deviation of the low-level data measurements is used as the estimate of the parameter σ_e.

7. **(Currently amended):** The method of claim 2 ~~claim 1~~, wherein a mean of negative control data is used as the estimate of the background parameter, α.

8. **(Currently amended):** The method of claim 2 ~~claim 1~~, wherein the biological molecule is a nucleic acid.

9. (Original): The method of claim 8, wherein the nucleic acid is mRNA.

10. (Original): The method of claim 8, wherein the biological molecule is DNA.

11. (Original): The method of claim 10, wherein the DNA is cDNA.

12. (Original): The method of claim 10, wherein the DNA is genomic.

13. (Canceled)

14. (Canceled)